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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/855,402A

DATE: 09/10/2001

TIME: 08:10:33

Input Set : A:\Bradfiel.app

Output Set: N:\CRF3\09102001\H855402A.raw

3 <110> APPLICANT: Bradfield, Christopher A.  
 4 Dolwick, Kristin M.  
 5 Carver, Lucy A.  
 7 <120> TITLE OF INVENTION: Ah Receptor cDNAs and Genetically Engineered Cells for  
 8 Detecting Agonists to the Ah Receptor  
 10 <130> FILE REFERENCE: HYBRIDZYME  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/08/855,402A  
 C--> 13 <141> CURRENT FILING DATE: 1997-05-13  
 15 <160> NUMBER OF SEQ ID NOS: 40  
 17 <170> SOFTWARE: PatentIn Ver. 2.1  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 3207  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: murine  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: CDS  
 26 <222> LOCATION: (1)..(2415)  
 28 <400> SEQUENCE: 1  
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 30 Met Ser Ser Gly Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg Lys  
 31 1 5 10 15  
 33 ccg gtg cag aaa aca gta aag ccc atc ccc gct gaa gga att aag tca 96  
 34 Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys Ser  
 35 20 25 30  
 37 aat cct tct aag cga cac aga gac cgg ctg aac aca gag tta gac cgc 144  
 38 Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp Arg  
 39 35 40 45  
 41 ctg gcc agc ctg ctg ccc ttc ccg caa gat gtt att aat aag ctg gac 192  
 42 Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu Asp  
 43 50 55 60  
 45 aaa ctc tct gtt agg ctc agc gtc acg tac ctg agg gcc aag agc 240  
 46 Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr Leu Arg Ala Lys Ser  
 47 65 70 75 80  
 49 ttc ttt gat gtt gca tta aag tcc acc cct gct gac aga aat gga ggc 288  
 50 Phe Phe Asp Val Ala Leu Lys Ser Thr Pro Ala Asp Arg Asn Gly Gly  
 51 85 90 95  
 53 cag gac cag tgt aga gca caa atc aga gac tgg cag gat ttg caa gaa 336  
 54 Gln Asp Gln Cys Arg Ala Gln Ile Arg Asp Trp Gln Asp Leu Gln Glu  
 55 100 105 110  
 57 gga gag ttc ttg tta cag gcg ctg aat ggc ttt gtg ctg gtt gtc aca 384  
 58 Gly Glu Phe Leu Leu Gln Ala Leu Asn Gly Phe Val Leu Val Val Thr  
 59 115 120 125  
 61 gca gat gcc ttg gtc ttc tat gct tcc act atc caa gat tac ctg 432  
 62 Ala Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp Tyr Leu  
 63 130 135 140  
 65 ggc ttt cag cag tct gat gtc atc cat cag agc gta tat gag ctc atc 480  
 66 Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val Tyr Glu Leu Ile

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10.5

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67	145	150	155	160	
69	cat aca gaa gac cgg gcg gaa ttc cag cgc cag ctt cac tgg gct cta				528
70	His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln Leu His Trp Ala Leu				
71	165	170	175		
73	aac cca gac tct gca caa gga gtg gac gaa gcc cat ggc cct cca cag				576
74	Asn Pro Asp Ser Ala Gln Gly Val Asp Glu Ala His Gly Pro Pro Gln				
75	180	185	190		
77	gca gca gtc tat tat acc cca gac cag ctt cct cca gag aac gct tct				624
78	Ala Ala Val Tyr Tyr Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser				
79	195	200	205		
81	ttc atg gag agg tgc ttc agg tgc cgg ctg agg tgc ctg gat aat				672
82	Phe Met Glu Arg Cys Phe Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn				
83	210	215	220		
85	tca tct ggt ttt ctg gca atg aat ttc caa ggg agg tta aag tat ctt				720
86	Ser Ser Gly Phe Leu Ala Met Asn Phe Gln Gly Arg Leu Lys Tyr Leu				
87	225	230	235	240	
89	cat gga cag aac aag aaa ggg aag gac gga gcg ctg ctt cct cca caa				768
90	His Gly Gln Asn Lys Lys Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln				
91	245	250	255		
93	ctg gct ttg ttt gca ata gct act cca ctt cag cca ccc tcc atc ctg				816
94	Leu Ala Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu				
95	260	265	270		
97	gaa att cga acc aaa aac ttc atc ttg agg acc aaa cac aag cta gac				864
98	Glu Ile Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp				
99	275	280	285		
101	ttc aca cct att ggt tgt gat gcc aaa ggg cag ctt att ctg ggc tat				912
102	Phe Thr Pro Ile Gly Cys Asp Ala Lys Gly Gln Leu Ile Leu Gly Tyr				
103	290	295	300		
105	aca gaa gta gag ctg tgc aca aga gga tcg ggg tac cag ttc atc cat				960
106	Thr Glu Val Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His				
107	305	310	315	320	
109	gct gca gac ata ctt cac tgt gca gaa tcc cac atc cgc atg att aag				1008
110	Ala Ala Asp Ile Leu His Cys Ala Glu Ser His Ile Arg Met Ile Lys				
111	325	330	335		
113	act gga gaa agt ggc atg aca gtt ttc cgg ctt ctt gca aaa cac agt				1056
114	Thr Gly Glu Ser Gly Met Thr Val Phe Arg Leu Leu Ala Lys His Ser				
115	340	345	350		
117	cgc tgg agg tgg gtc cag tcc aat gca cgc ttg att tac aga aat gga				1104
118	Arg Trp Arg Trp Val Gln Ser Asn Ala Arg Leu Ile Tyr Arg Asn Gly				
119	355	360	365		
121	aga cca gat tac atc atc gcc act cag aga cca ctg acg gat gaa gaa				1152
122	Arg Pro Asp Tyr Ile Ile Ala Thr Gln Arg Pro Leu Thr Asp Glu Glu				
123	370	375	380		
125	gga cga gag cat tta cag aag cga agt acg tcg ctg ccc ttc atg ttt				1200
126	Gly Arg Glu His Leu Gln Lys Arg Ser Thr Ser Leu Pro Phe Met Phe				
127	385	390	395	400	
129	gct acc gga gag gct gtg ttg tac gag atc tcc agc cct ttc tct ccc				1248
130	Ala Thr Gly Glu Ala Val Leu Tyr Glu Ile Ser Ser Pro Phe Ser Pro				
131	405	410	415		

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133	ata	atg	gat	ccc	cta	cca	ata	cgc	acc	aaa	agc	aac	act	agc	agg	aaa	1296
134	Ile	Met	Asp	Pro	Leu	Pro	Ile	Arg	Thr	Lys	Ser	Asn	Thr	Ser	Arg	Lys	
135				420				425							430		
137	gac	tgg	gct	ccc	cag	tca	acc	cca	agt	aag	gat	tct	tcc	cac	ccc	agt	1344
138	Asp	Trp	Ala	Pro	Gln	Ser	Thr	Pro	Ser	Lys	Asp	Ser	Phe	His	Pro	Ser	
139				435				440							445		
141	tct	ctt	atg	agt	gcc	ctc	atc	cag	cag	gat	gag	tcc	atc	tat	ctg	tgt	1392
142	Ser	Leu	Met	Ser	Ala	Leu	Ile	Gln	Gln	Asp	Glu	Ser	Ile	Tyr	Leu	Cys	
143				450				455							460		
145	cct	cct	tca	agc	cct	gcg	ctg	tta	gac	agc	cat	ttt	ctc	atg	ggc	tcc	1440
146	Pro	Pro	Ser	Ser	Pro	Ala	Leu	Leu	Asp	Ser	His	Phe	Leu	Met	Gly	Ser	
147	465				470						475				480		
149	gtg	agc	aag	tgc	ggg	agt	tgg	caa	gac	agc	ttt	gcg	gcc	gca	gga	agt	1488
150	Val	Ser	Lys	Cys	Gly	Ser	Trp	Gln	Asp	Ser	Phe	Ala	Ala	Ala	Gly	Ser	
151					485				490						495		
153	gag	gct	gcg	ctg	aaa	cat	gag	caa	att	gac	cat	gct	cag	gac	gtg	aac	1536
154	Glu	Ala	Ala	Leu	Lys	His	Glu	Gln	Ile	Gly	His	Ala	Gln	Asp	Val	Asn	
155				500				505							510		
157	ctt	gca	ctc	tct	ggc	ggc	ccc	tca	gag	ctc	ttt	ccg	gat	aat	aaa	aat	1584
158	Leu	Ala	Leu	Ser	Gly	Gly	Pro	Ser	Glu	Leu	Phe	Pro	Asp	Asn	Lys	Asn	
159				515				520							525		
161	aat	gac	ttg	tac	agc	atc	atg	agg	aac	ctt	ggg	att	gat	ttt	gaa	gat	1632
162	Asn	Asp	Leu	Tyr	Ser	Ile	Met	Arg	Asn	Leu	Gly	Ile	Asp	Phe	Glu	Asp	
163				530				535							540		
165	atc	aga	agc	atg	cag	aac	gag	gag	ttc	ttc	aga	act	gac	tcc	acc	gct	1680
166	Ile	Arg	Ser	Met	Gln	Asn	Glu	Glu	Phe	Phe	Arg	Thr	Asp	Ser	Thr	Ala	
167	545				550						555				560		
169	gct	ggt	gag	gtt	gac	ttc	aaa	gac	atc	gac	ata	acg	gac	gaa	atc	ctg	1728
170	Ala	Gly	Glu	Val	Asp	Phe	Lys	Asp	Ile	Asp	Ile	Thr	Asp	Glu	Ile	Leu	
171					565				570						575		
173	acc	tac	gtg	cag	gat	tcc	ctg	aac	aat	tca	act	ttg	ctg	aac	tcg	gct	1776
174	Thr	Tyr	Val	Gln	Asp	Ser	Leu	Asn	Asn	Ser	Thr	Leu	Leu	Asn	Ser	Ala	
175				580				585							590		
177	tgc	cag	cag	cag	cct	gtg	act	cag	cac	cta	agc	tgt	atg	ctg	cag	gag	1824
178	Cys	Gln	Gln	Gln	Pro	Val	Thr	Gln	His	Leu	Ser	Cys	Met	Leu	Gln	Glu	
179				595				600							605		
181	cgc	ctg	caa	cta	gag	caa	cag	caa	cag	ctt	cag	cag	ccc	ccg	ccg	cag	1872
182	Arg	Leu	Gln	Leu	Glu	Gln	Gln	Gln	Gln	Leu	Gln	Gln	Pro	Pro	Pro	Gln	
183				610				615							620		
185	gct	ctg	gag	ccc	cag	cag	cag	ctg	tgt	cag	atg	gtg	tgc	ccc	cag	caa	1920
186	Ala	Leu	Glu	Pro	Gln	Gln	Leu	Cys	Gln	Met	Val	Cys	Pro	Gln	Gln		
187	625				630					635					640		
189	gat	ctg	ggt	ccg	aag	cac	acg	caa	atc	aac	ggc	acg	ttt	gca	agt	tgg	1968
190	Asp	Leu	Gly	Pro	Lys	His	Thr	Gln	Ile	Asn	Gly	Thr	Phe	Ala	Ser	Trp	
191					645				650						655		
193	aac	ccc	acc	cct	ccc	gtg	tct	ttc	aac	tgt	ccc	cag	cag	gaa	cta	aag	2016
194	Asn	Pro	Thr	Pro	Pro	Val	Ser	Phe	Asn	Cys	Pro	Gln	Gln	Glu	Leu	Lys	
195				660				665							670		
197	cac	tat	cag	ctc	ttt	tcc	agc	tta	cag	ggg	act	gct	cag	gaa	ttt	ccc	2064

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198 His Tyr Gln Leu Phe Ser Ser Leu Gln Gly Thr Ala Gln Glu Phe Pro  
199 675 680 685  
201 tac aaa cca gag gtg gac agt gtg cct tac aca cag aac ttt gct ccc 2112  
202 Tyr Lys Pro Glu Val Asp Ser Val Pro Tyr Thr Gln Asn Phe Ala Pro  
203 690 695 700  
205 tgt aat cag cct ctg ctt cca gaa cat tcc aag agt gtg cag ttg gac 2160  
206 Cys Asn Gln Pro Leu Leu Pro Glu His Ser Lys Ser Val Gln Leu Asp  
207 705 710 715 720  
209 ttc cct gga agg gat ttt gaa ccg tcc ctg cat ccc act act tct aat 2208  
210 Phe Pro Gly Arg Asp Phe Glu Pro Ser Leu His Pro Thr Thr Ser Asn  
211 725 730 735  
213 tta gat ttt gtc agt tgt tta caa gtt cct gaa aac caa agt cat ggg 2256  
214 Leu Asp Phe Val Ser Cys Leu Gln Val Pro Glu Asn Gln Ser His Gly  
215 740 745 750  
217 ata aac tca cag tcc gcc atg gtc agt cct cag gca tac tat gct ggg 2304  
218 Ile Asn Ser Gln Ser Ala Met Val Ser Pro Gln Ala Tyr Tyr Ala Gly  
219 755 760 765  
221 gcc atg tcc atg tat cag tgc cag cca ggg cca cag cgc acc cct gtg 2352  
222 Ala Met Ser Met Tyr Gln Cys Gln Pro Gly Pro Gln Arg Thr Pro Val  
223 770 775 780  
225 gac cag acg cag tac agc tct gaa att cca ggt tct cag gca ttc cta 2400  
226 Asp Gln Thr Gln Tyr Ser Ser Glu Ile Pro Gly Ser Gln Ala Phe Leu  
227 785 790 795 800  
229 agc aag gtg cag agt tgaggtgttt tcaatgaaac ctattcgtcc gacttgagca 2455  
230 Ser Lys Val Gln Ser  
231 805  
233 gcattggcca cgctgctcag accactggcc atctccatca ctgcggaagc ccggcctctt 2515  
235 cccgatatac caccgggtgg attcctgttag ctcccatgcc aggatgaaat tcattcagga 2575  
237 acaggatacc agaactgtga ggggtggaca tcagtagact ttctccaaaa cagattcga 2635  
239 ttcttgtgtt tagagaagga gtttaaaacc cgtacactgat atgctcccta tacatggga 2695  
241 gagctcggac ggagcacatg ggaggagtgc aggacaccta gagtgcacag tgtttactgt 2755  
243 gaaaaattct cgggttccct gctcgttaac ttccagcagga aaaacagggg ggtatggaa 2815  
245 gctttgaact tctggattct tgtagtata ccaaatacgg agttacagga ctaaccgatt 2875  
247 toctatattt tttaacctct gttttgtcc cagaagttaa agtaaatggg ttggtgcttt 2935  
249 tctcaaaaga aaatctcaat gctttcttc tgcactgtta atataagtgc ctcacttttt 2995  
251 gttgttggttt ttgttggttt ctgattttt tcttttttc tatctacccgtaacacaata 3055  
253 ggttatgtat ttatatgaa atattttta tctttttga attaataattc ttctgcaca 3115  
255 aagaaaagttt cccgaatccc aacctttcta tgaccccgct gtgtgtgtgc actactcatc 3175  
257 ctttccttca gataaaaggt aattgataac tc 3207  
260 <210> SEQ ID NO: 2  
261 <211> LENGTH: 805  
262 <212> TYPE: PRT  
263 <213> ORGANISM: murine  
265 <400> SEQUENCE: 2  
266 Met Ser Ser Gly Ala Asn Ile Thr Tyr Ala Ser Arg Lys Arg Arg Lys  
267 1 5 10 15  
269 Pro Val Gln Lys Thr Val Lys Pro Ile Pro Ala Glu Gly Ile Lys Ser  
270 20 25 30  
272 Asn Pro Ser Lys Arg His Arg Asp Arg Leu Asn Thr Glu Leu Asp Arg

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273	35	40	45	
275	Leu Ala Ser Leu Leu Pro Phe Pro Gln Asp Val Ile Asn Lys Leu Asp			
276	50	55	60	
278	Lys Leu Ser Val Leu Arg Leu Ser Val Thr Tyr Leu Arg Ala Lys Ser			
279	65	70	75	80
281	Phe Phe Asp Val Ala Leu Lys Ser Thr Pro Ala Asp Arg Asn Gly Gly			
282	85	90	95	
284	Gln Asp Gln Cys Arg Ala Gln Ile Arg Asp Trp Gln Asp Leu Gln Glu			
285	100	105	110	
287	Gly Glu Phe Leu Leu Gln Ala Leu Asn Gly Phe Val Leu Val Val Thr			
288	115	120	125	
290	Ala Asp Ala Leu Val Phe Tyr Ala Ser Ser Thr Ile Gln Asp Tyr Leu			
291	130	135	140	
293	Gly Phe Gln Gln Ser Asp Val Ile His Gln Ser Val Tyr Glu Leu Ile			
294	145	150	155	160
296	His Thr Glu Asp Arg Ala Glu Phe Gln Arg Gln Leu His Trp Ala Leu			
297	165	170	175	
299	Asn Pro Asp Ser Ala Gln Gly Val Asp Glu Ala His Gly Pro Pro Gln			
300	180	185	190	
302	Ala Ala Val Tyr Tyr Thr Pro Asp Gln Leu Pro Pro Glu Asn Ala Ser			
303	195	200	205	
305	Phe Met Glu Arg Cys Phe Arg Cys Arg Leu Arg Cys Leu Leu Asp Asn			
306	210	215	220	
308	Ser Ser Gly Phe Leu Ala Met Asn Phe Gln Gly Arg Leu Lys Tyr Leu			
309	225	230	235	240
311	His Gly Gln Asn Lys Lys Gly Lys Asp Gly Ala Leu Leu Pro Pro Gln			
312	245	250	255	
314	Leu Ala Leu Phe Ala Ile Ala Thr Pro Leu Gln Pro Pro Ser Ile Leu			
315	260	265	270	
317	Glu Ile Arg Thr Lys Asn Phe Ile Phe Arg Thr Lys His Lys Leu Asp			
318	275	280	285	
320	Phe Thr Pro Ile Gly Cys Asp Ala Lys Gly Gln Leu Ile Leu Gly Tyr			
321	290	295	300	
323	Thr Glu Val Glu Leu Cys Thr Arg Gly Ser Gly Tyr Gln Phe Ile His			
324	305	310	315	320
326	Ala Ala Asp Ile Leu His Cys Ala Glu Ser His Ile Arg Met Ile Lys			
327	325	330	335	
329	Thr Gly Glu Ser Gly Met Thr Val Phe Arg Leu Leu Ala Lys His Ser			
330	340	345	350	
332	Arg Trp Arg Trp Val Gln Ser Asn Ala Arg Leu Ile Tyr Arg Asn Gly			
333	355	360	365	
335	Arg Pro Asp Tyr Ile Ile Ala Thr Gln Arg Pro Leu Thr Asp Glu Glu			
336	370	375	380	
338	Gly Arg Glu His Leu Gln Lys Arg Ser Thr Ser Leu Pro Phe Met Phe			
339	385	390	395	400
341	Ala Thr Gly Glu Ala Val Leu Tyr Glu Ile Ser Ser Pro Phe Ser Pro			
342	405	410	415	
344	Ile Met Asp Pro Leu Pro Ile Arg Thr Lys Ser Asn Thr Ser Arg Lys			
345	420	425	430	

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**

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L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6